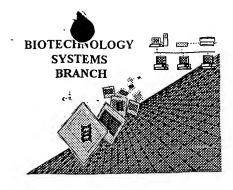
RAW SEQUENCE LISTING ERROR REPORT



#6 L. WITE

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/856,6/7Source: 9/856,6/7Date Processed by STIC: 9/856,6/7

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/856,617

DATE: 06/12/2001 TIME: 12:25:27

Input Set : A:\766.52 Seq. Listing.txt Output Set: N:\CRF3\06122001\1856617.raw

- 4 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD.,
- 6 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDE
- 8 <130> FILE REFERENCE: 11169
- C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/856,617
- C--> 11 <141> CURRENT FILING DATE: 2001-05-24
 - 13 <150> PRIOR APPLICATION NUMBER: H10-332484
 - 14 <151> PRIOR FILING DATE: 1998-11-24
 - 16 <150> PRIOR APPLICATION NUMBER: H11-248442
 - 17 <151> PRIOR FILING DATE: 1999-09-02
 - 19 <160> NUMBER OF SEQ ID NOS: 18
 - 20 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply Corrected Diskette Needed

ERRORED SEQUENCES

- 22 <210> SEQ ID NO: 1
- 23 <211> LENGTH: 4173
- 24 <212> TYPE: DNA
- 25 <213> ORGANISM: Mouse
- 27 <220> FEATURE:
- 28 <221> NAME/KEY: CDS
- 29 <222> LOCATION: (107)..(4021)
- 31 <400> SEQUENCE: 1

E--> 32 ggcctgggcg gcggcacatc ctaaggtagc ggctgcctga ggtgacagct gcccgtggat

E--> 35 tegggeeeeg gaacgageeg egetggegge ggeggeggta geegeg atg atg gag

36 115

37

38

E--> 40 atc cag atg gac gag gga ggt gtg gtg gtg tac caa gac gac tac

42 Ile Gln Met Asp Glu Gly Gly Val Val Val Tyr Gln Asp Asp Tyr

E--> 45 tgc tcg ggc tcg gtc atg tcg gag cgt gtg tcg ggc ctg gcg ggc tcc 46 211

47 Cys Ser Gly Ser Val Met Ser Glu Arq Val Ser Gly Leu Ala Gly Ser 48 20

E--> 50 atc tac cgc gag ttc gag cgc ctc att cac tgc tat gac gag gag gtg

52 Ile Tyr Arg Glu Phe Glu Arg Leu Ile His Cys Tyr Asp Glu Glu Val

E--> 55 gtc aag gag ctc atg ccg ctg gtg gtg aac gtg ctg gag aac ctt gac

56 307

57 Val Lys Glu Leu Met Pro Leu Val Val Asn Val Leu Glu Asn Leu Asp

60

E--> 60 tog gtg ctg agc gag aac cag gag cac gag gtg gag ctg gag ctc cta

61 355

Met Met Glu

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Input Set : A:\766.52 Seq. Listing.txt
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62 Ser Val Leu Ser Glu Asn Gln Glu His Glu Val Glu Leu Glu Leu 70 E--> 65 cgc gag gac aac gag cag ctg ctc acg caa tac gag cgc gag aag qcg 66 403 67 Arg Glu Asp Asn Glu Gln Leu Leu Thr Gln Tyr Glu Arg Glu Lys Ala 90 E--> 70 ctg cgc aaa cag gcc gag gag aaa ttc atc gaa ttt gaa gat gcc ttg 71 451 72 Leu Arg Lys Gln Ala Glu Glu Lys Phe Ile Glu Phe Glu Asp Ala Leu E--> 75 gaa caa gag aag aaa gaa ctc cag atc cag gta gaa cat tat gag ttt 76 499 77 Glu Gln Glu Lys Lys Glu Leu Gln Ile Gln Val Glu His Tyr Glu Phe 125 E--> 80 cag aca cgc cag ctg gag cta aag gcc aaa aac tat gca gat cag att 82 Gln Thr Arg Gln Leu Glu Leu Lys Ala Lys Asn Tyr Ala Asp Gln Ile 135 140 E--> 85 tcc cga ctg gag gaa cga gaa tcg gag atg aag aag gaa tac aat gcc 86 595 87 Ser Arg Leu Glu Glu Arg Glu Ser Glu Met Lys Lys Glu Tyr Asn Ala 150 155 E--> 90 ctg cac cag cgg cac aca gag atg atc cag acc tat gtg gaa cac att 91 643 92 Leu His Gln Arg His Thr Glu Met Ile Gln Thr Tyr Val Glu His Ile E--> 95 gaa aga tcc aag atg cag caa gtt ggg ggt agc ggc caa aca gaa agc 96 691 97 Glu Arg Ser Lys Met Gln Gln Val Gly Gly Ser Gly Gln Thr Glu Ser E--> 100 ago ctg ccc ggg cgg agg aag gag cgt ccc acc tct ctg aat gtc ttc 102 Ser Leu Pro Gly Arg Arg Lys Glu Arg Pro Thr Ser Leu Asn Val Phe E--> 105 ccc ctg gct gat ggc atg tgt cca aac gat gag atg tct gag tca ggc 106 787 107 Pro Leu Ala Asp Gly Met Cys Pro Asn Asp Glu Met Ser Glu Ser Gly E--> 110 cag tee tea gea get gea aca eee agt ace àca ggt ace aag tee aac 111 835 112 Gln Ser Ser Ala Ala Ala Thr Pro Ser Thr Thr Gly Thr Lys Ser Asn E--> 115 aca ccc acg tcc tcc gtg ccc tca gca gca gtc acg cca ctc aac gag 116 883 117 Thr Pro Thr Ser Ser Val Pro Ser Ala Ala Val Thr Pro Leu Asn Glu 250 E--> 120 agc cta cag ccc ctg ggg gac tat gtc agt gtc aca aag aac aag 121 931 122 Ser Leu Gln Pro Leu Gly Asp Tyr Val Ser Val Thr Lys Asn Asn Lys

sure



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Input Set : A:\766.52 Seq. Listing.txt
Output Set: N:\CRF3\06122001\1856617.raw

		260				265					270					275
E>		cag gcc 979	cga	gag	aag	cgc	aat	agc	cgt	aac	atg	gag	gtc	cag	gtc	acc
		Gln Ala	λνα	Clu	Two	λκα	λan	Sor	λνα	λαn	Mot	Gl n	Val	Gln	V = 1	Thr
	128	GIII AIA	ALY	GIU	280	Arg	ASII	261	Arg	285	Mec	GIU	Vai	GIII	290	1111
E>		caa gag	ato	caa		atc	agt.	atc	aac		aac	agc	agt	gac		taa
_ ,		1027	,	,	uuo	9.00	-5-		990		22~	9-	-5-	940	545	-99
		Gln Glu	Met	Arq	Asn	Val	Ser	Ile	Gly	Met	Gly	Ser	Ser	Asp	Glu	Trp
	133			295					300		-			305		-
E>	135	tcc gat	gtt	cag	gac	att	atc	gac	tcc	acc	cca	gag	ctg	gat	gtg	tgt
	136	1075														
	137	Ser Asp	Val	Gln	Asp	Ile	Ile	Asp	Ser	Thr	Pro	Glu	Leu	Asp	Val	Cys
	138		310					315					320			
E>		cct gaa	acc	cgt	ctg	gag	cgc	aca	gga	agc	agc	cca	acc	cag	gga	att
-		1123	en 1.	_	_	a 3	_	ml	a 1	a	a	5	m 1	01	01	-1 -
	142	Pro Glu 325		Arg	Leu	Glu	Arg	Tnr	GLY	Ser	ser	335	Thr	GIn	GIĀ	ше
F>		gta aac		aat	+++	aa s		220	act	424	tac		tat	Cac	maa.	ctc
F>		1171	aaa	gct		gga	acc	aac	acc	gac	LCC	ccg	Luc	cac	gaa	C C C
		Val Asn	Lys	Ala	Phe	Gly	Ile	Asn	Thr	Asp	Ser	Leu	Tyr	His	Glu	Leu
		340	•			345				-	350		-			355
E>	150	tcc acg	gcg	gga	tct	gag	gtc	atc	ggg	gat	gtg	gac	gag	gga	gct	gat
		1219														
		Ser Thr	Ala	Gly		Glu	Val	Ile	Gly	_	Val	Asp	Glu	Gly		Asp
	153				360					365					370	
E>		ctc cta 1267	ggg	gag	τττ	tca	gtg	cgc	gat	gat	דננ	דדד	gga	atg	ggc	aaa
		Leu Leu	Glv	Glu	Phe	Ser	Va l	Δra	Δsn	Δsn	Dhe	Dhe	Glv	Met	Glv	Lvs
	158	neu neu	011	375	1110	DCI	, 41	2129	380	шр	1110	1 110	011	385	011	
E>	160	gaa gtg	ggg	aac	ctg	ctg	ctg	gag	aac	tca	cag	ctt	cta	gag	aca	aaa
		1315														
		Glu Val	_	Asn	Leu	Leu	Leu		Asn	Ser	Gln	Leu	Leu	Glu	Thr	Lys
	163	-	390					395					400			
E>		aat gct	tta	aat	gta	gtg	aag	aat	gac	ctc	att	gct	aag	gtt	gac	caa
		1363	T OU	7 an	175.1	37 - 1	T *** G	7:an	N an	T 011	т1.	7 J -	T	17.2.1	7 an	Cln
	168	Asn Ala	цец	ASII	val	val	цуS 410	ASII	ASP	Leu	116	415	гу	Val	ASP	GTII
E>		ctg tca	σσа	σаа	саσ	σаσ	-	cta	aaσ	aat.	σaσ		gaa	gca	acc	ааσ
		1411	,,,-	J	5	J-J	J	,		<i></i>	J J		J	J	J	
	172	Leu Ser	Gly	Glu	Gln	Glu	Val	Leu	Lys	Gly	Glu	Leu	Glu	Ala	Ala	Lys
	173					425					430					435
E>		caa gcg	aaa	gtc	aag	ctg	gag	aac	cga	atc	aaa	gag	ctt	gaa	gaa	gaa
		1459	_		_	_		_	_	1	_	~ 7	_		~ 3	
		Gln Ala	Lys	Val	_	Leu	Glu	Asn	Arg		Lys	GLu	Leu	Glu		ĢĽu
F>	178	ctg aag	242	ata	440	tca	T2T	ac =	αt>	445	acc.	cac	ca+	asa	450	arra
F>		1507	aya	gic	aay	cca	yay	gea	yca	act	guu	cyc	cyt	yay		aya
		Leu Lys	Arg	Val	Lys	Ser	Glu	Ala	Val	Thr	Ala	Arg	Arq	Glu	Pro	Arg
	183	-	,	455	-				460			-		465		-

some of the same



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E--> 185 gaa gag gtg gag gat gta agc agc tat ctc tgt aca gaa ttg gac aaa 186 1555 187 Glu Glu Val Glu Asp Val Ser Ser Tyr Leu Cys Thr Glu Leu Asp Lys E--> 190 atc ccc atg gcc cag cgc cga cgc ttc aca cgg gtg gag atg gcc cga 191 1603 192 Ile Pro Met Ala Gln Arg Arg Phe Thr Arg Val Glu Met Ala Arg 490 E--> 195 gtg ctc atg gaa cgc aac cag tac aag gaa cgc ctc atg gag ctg cag 197 Val Leu Met Glu Arg Asn Gln Tyr Lys Glu Arg Leu. Met Glu Leu Gln 198 500 E--> 200 gag gct gtg agg tgg act gaa atg atc aga gca tca agg gaa cac cca 201 1699 202 Glu Ala Val Arg Trp Thr Glu Met Ile Arg Ala Ser Arg Glu His Pro 520 E--> 205 tot gto cag gag aag aag too acc atc tgg cag tto ttt agt cgc 206 1747 207 Ser Val Gln Glu Lys Lys Lys Ser Thr Ile Trp Gln Phe Phe Ser Arg 208 540 E--> 210 ctc ttc agc tcc tca tct agc ccc cct ccg gcc aaa cga tcc tac cca 211 1795 212 Leu Phe Ser Ser Ser Ser Pro Pro Pro Ala Lys Arg Ser Tyr Pro E--> 215 tot gtg aac att cac tac aag toa coc act gca gct ggc ttt agc cag 216 1843 217 Ser Val Asn Ile His Tyr Lys Ser Pro Thr Ala Ala Gly Phe Ser Gln 565 E--> 220 cgt cgc agc cat gct ttg tgc cag atc tca gcc ggc agc agg ccc ctg 221 1891 222 Arg Arg Ser His Ala Leu Cys Gln Ile Ser Ala Gly Ser Arg Pro Leu E--> 225 gag ttc ttc cct gat gat gac tgc acc tct tct gcc cgg cgg gag cag 226 1939 227 Glu Phe Phe Pro Asp Asp Cys Thr Ser Ser Ala Arg Arg Glu Gln 228 600 605 E--> 230 aag cgg gag cag tac cgc cag gtt cgt gaa cac gtg cgc aat gat gac 232 Lys Arg Glu Gln Tyr Arg Gln Val Arg Glu His Val Arg Asn Asp Asp E--> 235 ggg agg ctg cag gcc tgt ggg tgg agc ctg cct gcc aag tac aag cag 237 Gly Arg Leu Gln Ala Cys Gly Trp Ser Leu Pro Ala Lys Tyr Lys Gln 635 630 E--> 240 ctg agc ccc aat gga ggc cag gaa gac acc cgg atg aaa aat gtg cct 241 2083 242 Leu Ser Pro Asn Gly Gly Gln Glu Asp Thr Arg Met Lys Asn Val Pro 243 645 650

some

Sue size of enough of sheet pager shown as sample of

FYI Please review the

Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

E--> 245 gtc cct gtg tac tgt cgc cct ctg gtg gag aag gac cct tcg aca aag